

SEQUENCE LISTING

[0355] A sequence listing transmittal sheet and a sequence listing in paper format accompanies this application.

SEQ. ID. NO.:1 HG1015090N1 CLN00493987_5pvl.a

ATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTGCTTCTCTGGA GCCAGGTATCA
GGGGCCCAGGGCCAAGAATTCCACTTTGGGGCCCTGCCAAGTGAAGGGGGTTGTTCCCCAG
AAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGATAACATCACG
AGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGCTGTTAC
CTTGTCCACACCCTGCTGGAGTTCTACTTGAAAAGTGTTCATAAACTACCACAATAGA
ACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACCTTTGTTCTCATC
GTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACAC
AGGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACC
AAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGCTCTGA

SEQ. ID. NO.:2 HG1015091N1 NP_006841:NM_006850

ATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTCCT
TTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTG
CTTCTCTGGAGCCAGGTATCAGGGGGCCCAGGGCCAAGAATTCCACTTTGGGGCCCTGCCAA
GTGAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATG
CAAGCTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTC
TCGGATGCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAAGTGT
TTCAAAAAGTACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTG
GCCAACAACCTTTGTTCTCATCGTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTT
TCCATCAGAGACAGTGCACACAGGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTG
GACGTAGAAGCAGCTCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATG
CAGAAATTCTACAAGCTCTGA

SEQ. ID. NO.:3 HG1015092N1 CLN00453866_5pvl.a

ATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTGCTTCTCTGGA GCCAGGTATCA
GGGGCCCAGGGCCAAGAATTCCACTTTGGGGCCCTGCCAAGTGAAGGGGGTTGTTCCCCAG
AAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGATAACATCACG
AGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGCAAGAAAATGAGATGTTT
TCCATCAGAGACAGTGCACACAGGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTG
GACGTAGAAGCAGCTCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATG
CAGAAATTCTACAAGCTCTGA

SEQ. ID. NO.:4 HG1015093N1 NP_006841:NM_006850_exon1

ATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAG

SEQ. ID. NO.:5 HG1015094N1 NP_006841:NM_006850_exon4

GATGCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAAGTGTTC
AAAAAGTACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCC
AACAACTTTGTTCTCATCGTGTCACAACTGCAACCCAGT

SEQ. ID. NO.:6 HG1015090P1 CLN00493987_5pvl.a

MQMVVLPCLGFTLLLWSQVSGAQQQEFHFGPCQVKGVVPQKLWEAFWAVKDTMQAQDNIT
SARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNYHNRTVEVRTLKSFSTLANNFVLI
VSQQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKALGEVDILLTWMQKFYKL

SEQ. ID. NO.:7 HG1015091P1 NP_006841:NM_006850

MNFQQRLLQSLWTLARPCPPLLATASQMOMVVLPCLGFTLLLWSQVSGAQQQEFHFGPCQ
VKGVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTV
FKNYHNRTVEVRTLKSFSTLANNFVLIVSQQPSQENEMFSIRDSAHRRFLLFRRAFKQL
DVEAALTKALGEVDILLTWMQKFYKL

SEQ. ID. NO.:8 HG1015092P1 CLN00453866_5pvl.a

MQMVVLPCLGFTLLLWSQVSGAQQQEFHFGPCQVKGVVPQKLWEAFWAVKDTMQAQDNIT

SARLLQQEVLQNVSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKALGEVDILLTWM
QKFYKL

SEQ. ID. NO.:9 HG1015093P1 NP_006841:NM_006850_exon1
MNFQQRQLQSLWTLA

SEQ. ID. NO.:10 HG1015094P1 NP_006841:NM_006850_exon4
DAESCYLVHTLLEFYLKTVFKNYHNRTVEVRTLKSFSTLANNFVLIVSQLQPS

SEQ. ID. NO.:11 HG1015090N0 CLN00493987_5pvl.a
TGACACTATAGACCCTGGCTTGCCTGCAAACCTTTACTTCTGAAATGACTTCCACGTCTG
GGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAATGGTGAAGGTGCCTGTC
TAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCCCTCAAGCATCACTTAC
AGGACCAGAGCAGACCCTTCTGCCCTCCTTTGCTGGCGACAGCCTCTCAAATGCAGATGG
TTGTGCTCCCTTGCCTGGGTTTTACCCTGCTTCTCTGGAGCCAGGTATCAGGGGGCCAGG
GCCAAGAATTCCACTTTGGGCCCTGCCAAGTGAAGGGGGTGTTCCTCCAGAACTGTGGG
AAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGATAACATCACGAGTGCCCGGC
TGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGCTGTTACCTTGTCCACA
CCCTGCTGGAGTTCTACTTGAAAACCTGTTTTCAAAAACCTACCACAATAGAACAAGTTGAAG
TCAGGACTCTGAAGTCATTCTCTACTCTGGCCAAACAACCTTTGTTCTCATCGTGTCAACA
TGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGGCGGTTTC
TGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGCCCTTG
GGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGCTCTGAATGTCTAGAC
CAGGACCTCCCTCCCCCTGGCACTGGG

SEQ. ID. NO.:12 HG1015091N0 NP_006841:NM_006850
CTTGCCTGCAAACCTTTACTTCTGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACC
CACAGCTATGCCTCTGATTGGTGAATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAG
AACCAGCTGCCTCCAGGCAGCCAGCCCTCAAGCATCACTTACAGGACCAGAGGGACAAGA
CATGACTGTGATGAGGAGCTGCTTTCCGCAATTTAACACCAAGAAGAATTGAGGCTGCTT
GGGAGGAAGGCCAGGAGGAACACGAGACTGAGAGATGAATTTTCAACAGAGGCTGCAAAAG
CCTGTGGACTTTAGCCAGACCCTTCTGCCCTCCTTTGCTGGCGACAGCCTCTCAAATGCA
GATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTGCTTCTCTGGAGCCAGGTATCAGGGGC
CCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGTGAAGGGGGTGTTCCTCCAGAACT
GTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGATAACATCACGAGTGC
CCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGCTGTTACCTTGT
CCACACCCTGCTGGAGTTCTACTTGAAAACCTGTTTTCAAAAACCTACCACAATAGAACAGT
TGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAAACAACCTTTGTTCTCATCGTGT
ACAACCTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGGCG
GTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGC
CCTTGGGGAAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGCTCTGAATGTC
TAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTTGTTCCCTGTGTCAATTTCAAACAGTCT
CCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTTCTTGGCC
CAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAGGTGC
CTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTAA
TTAATGTCAAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGC
AGTGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTG
GATTGTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACCTGAACCTTCAGAGCATGAAAAT
CACACTGTCTGCT

SEQ. ID. NO.:13 HG1015092N0 CLN00453866_5pvl.a
TATAGAACCAGGCTTGCCTGCAAACCTTTACTTCTGAAATGACTTCCACGGCTGGGACGG
GAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAATGGTGAAGGTGCCTGTCTAACTT
TTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCCCTCAAGCATCACTTACAGGACC
AGAGCAGACCCTTCTGCCCTCCTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGC
TCCCTTGCCTGGGTTTTACCCTGCTTCTCTGGAGCCAGGTATCAGGGGGCCAGGGCCAAG
AATTCCAACCTTGGGCCCTGCCAAGTGAAGGGGGTGTTCCTCCAGAACTGTGGGAAGCCT
TCTGGGCTGTGAAAGACACTATGCAAGCTCAGGATAACATCACGAGTGCCCGGCTGCTGC

AGCAGGAGGTTCTGCAGAACGTCTCGCAAGAAAATGAGATGTTTTCCATCAGAGACAGTG
CACACAGGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTC
TGACCAAAGCCCTTGGGGAAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGC
TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTT
CAAACAGTCTCCCTTCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCC
ATTCTTGGCCC

SEQ. ID. NO.:14 HG1014901N1 CLN00108891_5pvl.a

ATGGCTATGATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTG
ATCTTCACAGTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACCTTACGTGTACTTTACCAAC
GAGCTGAAGCAGATGATTTTGAGAACCTCTGAGGAAACCATTCTACAGTTCAAGAAAAG
CAACAAAATATTTCTCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCAGCTCACATA
ACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAATGAAAAGGCT
CTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTTCATTCTGAGCAAC
TTGCACTTGAGGAATGGTGAACCTGGTCATCCATGAAAAAGGGTTTTACTACATCTATTCC
CAAACATACTTTCGATTTTCAGGAGGAAATAAAAGAAAACACAAAGAACGACAAACAAATG
GTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATGAAAAGTGCT
AGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTGCATCTATCAAGGGGGA
ATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAGCACTTGATA
GACATGGACCATGAAGCCAGTTTTTTTCGGGGCCTTTTTAGTTGGCTAA

SEQ. ID. NO.:15 HG1014901P1 CLN00108891_5pvl.a

MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMILRTSEETISTVQEK
QQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSN
LHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKS
RNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG

SEQ. ID. NO.:16 HG1014901N0 CLN00108891_5pvl.a

GACCGGCTGCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGATCATGGCTATGATGGA
GGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGTGCT
CCTGCAGTCTCTCTGTGTGGCTGTAACCTTACGTGTACTTTACCAACGAGCTGAAGCAGAT
GATTTTGAGAACCTCTGAGGAAACCATTCTACAGTTCAAGAAAAGCAACAAAATATTTCT
TCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGG
AAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAATGAAAAGGCTCTGGGCCGCAAAAT
AACTCCTGGGAATCATCAAGGAGTGGGCATTTCATTCTGAGCAACTTGCATTGAGGAA
TGGTGAACCTGGTCATCCATGAAAAAGGGTTTTACTACATCTATTCCCAAACATACTTTCTG
ATTTTCAGGAGGAAATAAAAGAAAACACAAAGAACGACAAACAAATGGTCCAATATATTTA
CAAATACACAAGTTATCCTGACCCTATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTG
GTCTAAAGATGCAGAATATGGACTCTATTCCATCTATCAAGGGGGAATATTTGAGCTTAA
GGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAGCACTTGATAGACATGGACCATGA
AGCCAGTTTTTTTCGGGGCCTTTTTAGTTGGCTAACTGACCTGGAAAGAAAAGCAATAAC
CTCAAAGTGACTATTTCAGTTTTTCAGGATG

SEQ. ID. NO.:17 HG1019036N1 CLN00108891_frag1

ATTTTGAGAACCTCTGAGGAAACCATTCTACAGTTCAAGAAAAGCAACAAAATATTTCT
CCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGA
AGAAGCAACACATTGTCTTCTCCAAACTCCAAGAATGAAAAGGCTCTGGGCCGCAAAATA
AACTCCTGGGAATCATCAAGGAGTGGGCATTTCATTCTGAGCAACTTGCATTGAGGAAT
GGTGAACCTGGTCATCCATGAAAAAGGGTTTTACTACATCTATTCCCAAACATACTTTCTGA
TTTCAGGAGGAAATAAAAGAAAACACAAAGAACGACAAACAAATGGTCCAATATATTTAC
AAATACACAAGTTATCCTGACCCTATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGG
TCTAAAGATGCAGAATATGGACTCTATTCCATCTATCAAGGGGGAATATTTGAGCTTAA
GAAAATGACAGAATTTTTGTTTCTGTAACAAATGAGCACTTGATAGACATGGACCATGAA
GCCAGTTTTTTTCGGGGCCTTTTTAGTTGGC

SEQ. ID. NO.:18 HG1019037N1 CLN00108891_frag2

AACGAGCTGAAGCAGATGATTTTGAGAACCTCTGAGGAAACCATTCTACAGTTCAAGAA
AAGCAACAAAATATTTCTCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCAGCTCAC
ATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAATGAAAAG
GCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTTCATTCTGAGC

AACTTGCACTTGAGGAATGGTGAAGTGGTCATCCATGAAAAAGGGTTTTACTACATCTAT
TCCCAAACATACTTTTCGATTTTCAGGAGGAAATAAAAGAAAACACAAAGAACGACAAACAA
ATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATGAAAAGT
GCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTATCAAGGG
GGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTTCTGTAACAAATGAGCACTTG
ATAGACATGGACCATGAAGCCAGTTTTTTTCGGGGCCTTTTTAGTTGGC

SEQ. ID. NO.:19 HG1019038N1 NP_003801:NM_003810

ATGGCTATGATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTG
ATCTTCACAGTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACCTTACGTGTACTTTACCAAC
GAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTCTTAAAAGAA
GATGACAGTTATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTC
AAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATT
TCTACAGTTCAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAG
AGAGTAGCAGCTCACATAACTGGGACCAAGGAAGAAGCAACACATTGTCTTCTCCAAAC
TCCAAGAATGAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGG
CATTCACTCCTGAGCAACTTGCACCTTGAGGAATGGTGAAGTGGTCATCCATGAAAAAGGG
TTTTACTACATCTATTCCCAAACATACTTTTCGATTTTCAGGAGGAAATAAAAGAAAACACA
AAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATA
TTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTAT
TCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTTCTGTA
ACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTTCGGGGCCTTTTTAGTT
GGCTAA

SEQ. ID. NO.:20 HG1019040N1 CLN00108891_5pv1.a_frag1
GAGCTGAATGCAGATGATTTTGAGAACCTCT

SEQ. ID. NO.:21 HG1019036P1 CLN00108891_frag1

ILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKI
NSWESSRSGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIY
KYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHE
ASFFGAFLVG

SEQ. ID. NO.:22 HG1019037P1 CLN00108891_frag2

NELKQMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEK
ALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQ
MVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHL
IDMDHEASFFGAFLVG

SEQ. ID. NO.:23 HG1019038P1 NP_003801:NM_003810

MAMMEVQGGPSLGQTCVLIVFTVLLQSLCVAVTYVYFTNELKQMMDKYSGIACFLKE
DDSYWDPNDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQ
RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLY
SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG

SEQ. ID. NO.:24 HG1019040P1 CLN00108891_5pv1.a_frag1
ELKQMILRTS

SEQ. ID. NO.:25 HG1019038N0 NP_003801:NM_003810

TTTCATTTCTCACTGACTATAAAAGAATAGAGAAGGAAGGGCTTCAGTGACCGGCTGCC
TGGCTGACTTACAGCAGTCAGACTCTGACAGGATCATGGCTATGATGGAGGTCCAGGGGG
GACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGTGCTCCTGCAGTCTC
TCTGTGTGGCTGTAACCTTACGTGTACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGT
ACTCCAAAAGTGGCATTGCTTGTCTTAAAAGAAGATGACAGTTATTGGGACCCCAATG
ACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAACTCCGTCAGCTCGTTA
GAAAGATGATTTTGAGAACCTCTGAGGAAACCATTCTACAGTTCAAGAAAAGCAACAAA
ATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCAGCTCACATAACTGGGA
CCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAATGAAAAGGCTCTGGGCC
GCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCACTCCTGAGCAACTTGCACT

TGAGGAATGGTGAACCTGGTCATCCATGAAAAAGGGTTTTACTACATCTATTCCCAAACAT
ACTTTTCGATTTTCAGGAGGAAATAAAAAGAAAAACACAAAGAACGAACAAACAAATGGTCCAAT
ATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATGAAAAGTGCTAGAAATA
GTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTATCAAGGGGGGAATATTG
AGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAGCACTTGATAGACATGG
ACCATGAAGCCAGTTTTTTTCGGGGCCTTTTTAGTTGGCTAACTGACCTGGAAAGAAAAAG
CAATAACCTCAAAGTGACTATTCAGTTTTTCAGGATGATACACTATGAAGATGTTTCAAAA
AATCTGACCAAAACAAACAAACAGAAAACAGAAAACAAAAAAACCTCTATGCAATCTGAG
TAGAGCAGCCACAACCAAAAAATTCTACAACACACACTGTTCTGAAAGTGACTCACTTAT
CCCAAGAGAATGAAATTGCTGAAAGATCTTTCAGGACTCTACCTCATATCAGTTTGCTAG
CAGAAATCTAGAAGACTGTCAGCTTCCAACATTAATGCAATGGTTAACATCTTCTGTCT
TTATAATCTACTCCTTGTAAGACTGTAGAAGAAAGAGCAACAATCCATCTCTCAAGTAG
TGTATCACAGTAGTAGCCTCCAGGTTTCCTTAAGGGACAACATCCTTAAGTCAAAAGAGA
GAAGAGGCACCACTAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCC
AACATTTTGGGAACCCAAGGTGGGTAGATCACGAGATCAAGAGATCAAGACCATAGTGAC
CAACATAGTGAAACCCCATCTCTACTGAAAGTACAAAAATTAGCTGGGTGTGTTGGCACA
TGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGGCAAGAGAATTGTTTGAACCCGGGAGGC
AGAGGTTGCAGTGTGGTGTGAGATCATGCCACTACACTCCAGCCTGGCGACAGAGCGAGACT
TGGTTTCAAAAAAAAAAAAAAAAAAAAAAACTTCAGTAAGTACGTGTTATTTTTTTCAATAAA
ATTCTATTACAGTATGTCAAAAAAAAAAAAAAAAAAAAAA

SEQ. ID. NO.:26 HG1018265P1 collagen_leader_seq
MKTCWKIPVFFFVCSFLEPWASA

SEQ. ID. NO.:27 HG1018268P1 112907:21594845_1-17
MALLWGLLVLSWSCLQG

SEQ. ID. NO.:28 HG1018269P1 112907:21594845_1-13
MALLWGLLVLSWS

SEQ. ID. NO.:29 HG1018270P1 112907:21594845_1-19
MALLWGLLVLSWSCLQGPC

SEQ. ID. NO.:30 HG1018271P1 112907:21594845_1-16
MALLWGLLVLSWSCLQ

SEQ. ID. NO.:31 HG1018272P1 112907:21594845_1-15
MALLWGLLVLSWSCL

SEQ. ID. NO.:32 HG1018274P1 13325208:13325207_1-30
MDSMPEPASRCLLLLPLLLLLLLLLLPAPEL

SEQ. ID. NO.:33 HG1018275P1 13325208:13325207_1-25
MDSMPEPASRCLLLLPLLLLLLLLLL

SEQ. ID. NO.:34 HG1018276P1 13325208:13325207_1-33
MDSMPEPASRCLLLLPLLLLLLLLLLPAPELGPS

SEQ. ID. NO.:35 HG1018277P1 13325208:13325207_1-24
MDSMPEPASRCLLLLPLLLLLLLLLL

SEQ. ID. NO.:36 HG1018278P1 13325208:13325207_1-26
MDSMPEPASRCLLLLPLLLLLLLLLLP

SEQ. ID. NO.:37 HG1018279P1 13325208:13325207_1-32
MDSMPEPASRCLLLLPLLLLLLLLLLPAPELGP

SEQ. ID. NO.:38 HG1018280P1 13325208:13325207_1-27
MDSMPEPASRCLLLLPLLLLLLLLLLPA

SEQ. ID. NO.:39 HG1018281P1 13325208:13325207_1-23
MDSMPEPASRCLLLPLLLLLLL

SEQ. ID. NO.:40 HG1018282P1 13325208:13325207_1-35
MDSMPEPASRCLLLPLLLLLLLLLLPAPELGPSQA

SEQ. ID. NO.:41 HG1018284P1 13938307:13938306_1-24
MRRMWATQGLAVALALSVLPGSRA

SEQ. ID. NO.:42 HG1018285P1 13938307:13938306_1-21
MRRMWATQGLAVALALSVLPG

SEQ. ID. NO.:43 HG1018287P1 14718453:14718452_1-19
MDLRQFLMCLSLCTAFALS

SEQ. ID. NO.:44 HG1018288P1 14718453:14718452_1-15
MDLRQFLMCLSLCTA

SEQ. ID. NO.:45 HG1018289P1 14718453:14718452_1-17
MDLRQFLMCLSLCTAFA

SEQ. ID. NO.:46 HG1018291P1 15929966:15929965_1-23
MKTCWKIPVFFVCSFLEPWASA

SEQ. ID. NO.:47 HG1018293P1 16356651:16356650_1-21
MML RVLVGAVLPAML LAAPP

SEQ. ID. NO.:48 HG1018294P1 16356651:16356650_1-17
MML RVLVGAVLPAML LA

SEQ. ID. NO.:49 HG1018296P1 18204192:18204191_1-19
MRLSLPLLLLLLGAWAIPG

SEQ. ID. NO.:50 HG1018297P1 18204192:18204191_1-22
MRLSLPLLLLLLGAWAIPGGLG

SEQ. ID. NO.:51 HG1018298P1 18204192:18204191_1-18
MRLSLPLLLLLLGAWAIP

SEQ. ID. NO.:52 HG1018299P1 18204192:18204191_1-16
MRLSLPLLLLLLGAWA

SEQ. ID. NO.:53 HG1018300P1 18204192:18204191_1-14
MRLSLPLLLLLGA

SEQ. ID. NO.:54 HG1018302P1 23503038:15778555_1-20
MSML VVFLLLWGV TWGPVTE

SEQ. ID. NO.:55 HG1018303P1 23503038:15778555_1-16
MSML VVFLLLWGV TWG

SEQ. ID. NO.:56 HG1018304P1 23503038:15778555_1-21
MSML VVFLLLWGV TWGPVTEA

SEQ. ID. NO.:57 HG1018306P1 27479535:27479534_1-24
MRALRDRAGLLLCVLLLAALLEAA

SEQ. ID. NO.:58 HG1018307P1 27479535:27479534_1-20
MRALRDRAGLLLCVLLLAAL

SEQ. ID. NO.:59 HG1018308P1 27479535:27479534_1-26
MRALRDRAGLLLCVLLLAALLEAALG

SEQ. ID. NO.:60 HG1018309P1 27479535:27479534_1-21
MRALRDRAGLLLCVLLLAALL

SEQ. ID. NO.:61 HG1018310P1 27479535:27479534_1-23
MRALRDRAGLLLCVLLLAALLEA

SEQ. ID. NO.:62 HG1018312P1 37182960:37182959_1-24
MRAPGCGRLVLPPLLLAAAALAEG

SEQ. ID. NO.:63 HG1018313P1 37182960:37182959_1-19
MRAPGCGRLVLPPLLLAAA

SEQ. ID. NO.:64 HG1018314P1 37182960:37182959_1-22
MRAPGCGRLVLPPLLLAAAALA

SEQ. ID. NO.:65 HG1018315P1 37182960:37182959_1-20
MRAPGCGRLVLPPLLLAAAA

SEQ. ID. NO.:66 HG1018316P1 37182960:37182959_1-26
MRAPGCGRLVLPPLLLAAAALAEGDA

SEQ. ID. NO.:67 HG1018317P1 37182960:37182959_1-21
MRAPGCGRLVLPPLLLAAAAL

SEQ. ID. NO.:68 HG1018319P1 7437388:1208426_1-24
MRLRRLALFPGVALLAAGRLVAA

SEQ. ID. NO.:69 HG1018320P1 7437388:1208426_1-23
MRLRRLALFPGVALLAAGRLVA

SEQ. ID. NO.:70 HG1018322P1 NP_000286:NM_000295_1-24
MPSSVSWGILLLAGLCCCLVPVSLA

SEQ. ID. NO.:71 HG1018323P1 NP_000286:NM_000295_1-18
MPSSVSWGILLLAGLCCCL

SEQ. ID. NO.:72 HG1018324P1 NP_000286:NM_000295_1-23
MPSSVSWGILLLAGLCCCLVPVSL

SEQ. ID. NO.:73 HG1018325P1 NP_000286:NM_000295_1-17
MPSSVSWGILLLAGLCC

SEQ. ID. NO.:74 HG1018327P1 NP_000396:NM_000405_1-23
MQSLMQAPLLIALGLLLATPAQA

SEQ. ID. NO.:75 HG1018328P1 NP_000396:NM_000405_1-18
MQSLMQAPLLIALGLLLA

SEQ. ID. NO.:76 HG1018329P1 NP_000396:NM_000405_1-25
MQSLMQAPLLIALGLLLATPAQAH

SEQ. ID. NO.:77 HG1018330P1 NP_000396:NM_000405_1-20
MQSLMQAPLLIALGLLLATP

SEQ. ID. NO.:78 HG1018331P1 NP_000396:NM_000405_1-21
MQSLMQAPLLIALGLLLATPA

SEQ. ID. NO.:79 HG1018333P1 NP_000495:NM_000504_1-23
MGRPLHLVLLSASLAGLLLLGES

SEQ. ID. NO.:80 HG1018334P1 NP_000495:NM_000504_1-19
MGRPLHLVLLSASLAGLLL

SEQ. ID. NO.:81 HG1018335P1 NP_000495:NM_000504_1-20
MGRPLHLVLLSASLAGLLLL

SEQ. ID. NO.:82 HG1018336P1 NP_000495:NM_000504_1-15
MGRPLHLVLLSASLA

SEQ. ID. NO.:83 HG1018337P1 NP_000495:NM_000504_1-21
MGRPLHLVLLSASLAGLLLLG

SEQ. ID. NO.:84 HG1018338P1 NP_000495:NM_000504_1-17
MGRPLHLVLLSASLAGL

SEQ. ID. NO.:85 HG1018340P1 NP_000573:NM_000582_1-18
MRIAVICFCLLGITCAIP

SEQ. ID. NO.:86 HG1018341P1 NP_000573:NM_000582_1-16
MRIAVICFCLLGITCA

SEQ. ID. NO.:87 HG1018342P1 NP_000573:NM_000582_1-15
MRIAVICFCLLGITC

SEQ. ID. NO.:88 HG1018344P1 NP_000574:NM_000583_1-16
MKRVLVLLLAFAFGHA

SEQ. ID. NO.:89 HG1018345P1 NP_000574:NM_000583_1-14
MKRVLVLLLAFAFG

SEQ. ID. NO.:90 HG1018347P1 NP_000591:NM_000600_1-25
MNSFSTSAFGPVAFSLGLLLVLPAA

SEQ. ID. NO.:91 HG1018348P1 NP_000591:NM_000600_1-24
MNSFSTSAFGPVAFSLGLLLVLPA

SEQ. ID. NO.:92 HG1018349P1 NP_000591:NM_000600_1-27
MNSFSTSAFGPVAFSLGLLLVLPAAFP

SEQ. ID. NO.:93 HG1018351P1 NP_000598:NM_000607_1-18
MALSWVLTVLSLLPLEA

SEQ. ID. NO.:94 HG1018353P1 NP_000604:NM_000613_1-19
MARVLGAPVALGLWSLCWS

SEQ. ID. NO.:95 HG1018354P1 NP_000604:NM_000613_1-25
MARVLGAPVALGLWSLCWSLAIATP

SEQ. ID. NO.:96 HG1018355P1 NP_000604:NM_000613_1-21
MARVLGAPVALGLWSLCWSLA

SEQ. ID. NO.:97 HG1018356P1 NP_000604:NM_000613_1-23
MARVLGAPVALGLWSLCWSLAIA

SEQ. ID. NO.:98 HG1018357P1 NP_000604:NM_000613_1-31
MARVLGAPVALGLWSLCWSLAIATPLPPTSA

SEQ. ID. NO.:99 HG1018359P1 NP_000726:NM_000735_1-26
MDYYRKYAAIFLVTLSVFLHVLHSAP

SEQ. ID. NO.:100 HG1018360P1 NP_000726:NM_000735_1-24
MDYYRKYAAIFLVTLSVFLHVLHS

SEQ. ID. NO.:101 HG1018362P1 NP_000884:NM_000893_1-18
MKLITILFLCSRLLLSLT

SEQ. ID. NO.:102 HG1018363P1 NP_000884:NM_000893_1-19
MKLITILFLCSRLLLSLTQ

SEQ. ID. NO.:103 HG1018364P1 NP_000884:NM_000893_1-16
MKLITILFLCSRLLLS

SEQ. ID. NO.:104 HG1018365P1 NP_000884:NM_000893_1-23
MKLITILFLCSRLLLSLTQESQS

SEQ. ID. NO.:105 HG1018367P1 NP_000909:NM_000918_1-17
ML RRALLCLAVAALVRA

SEQ. ID. NO.:106 HG1018369P1 NP_000930:NM_000939_1-23
MPRSCCSRSGALLLALLLQASME

SEQ. ID. NO.:107 HG1018370P1 NP_000930:NM_000939_1-26
MPRSCCSRSGALLLALLLQASMEVRG

SEQ. ID. NO.:108 HG1018372P1 NP_000945:NM_000954_1-23
MATHHTLWMGLALLGVLDLQAA

SEQ. ID. NO.:109 HG1018373P1 NP_000945:NM_000954_1-22
MATHHTLWMGLALLGVLDLQA

SEQ. ID. NO.:110 HG1018374P1 NP_000945:NM_000954_1-18
MATHHTLWMGLALLGVLG

SEQ. ID. NO.:111 HG1018376P1 NP_001176:NM_001185_1-18
MVRMVPVLLSLLLLLGA

SEQ. ID. NO.:112 HG1018377P1 NP_001176:NM_001185_1-20
MVRMVPVLLSLLLLLGA

SEQ. ID. NO.:113 HG1018378P1 NP_001176:NM_001185_1-21
MVRMVPVLLSLLLLLGA

SEQ. ID. NO.:114 HG1018379P1 NP_001176:NM_001185_1-17
MVRMVPVLLSLLLLLGP

SEQ. ID. NO.:115 HG1018381P1 NP_001266:NM_001275_1-18
MRSAAVLALLCAGQVTA

SEQ. ID. NO.:116 HG1018382P1 NP_001266:NM_001275_1-15
MRSAAVLALLCAGQ

SEQ. ID. NO.:117 HG1018383P1 NP_001266:NM_001275_1-14
MRSAAVLALLCAG

SEQ. ID. NO.:118 HG1018385P1 NP_001314:NM_001323_1-26
MARNLPLALGLALVAFCLLALPRDA

SEQ. ID. NO.:119 HG1018386P1 NP_001314:NM_001323_1-18
MARSNLPLALGLALVAF C

SEQ. ID. NO.:120 HG1018387P1 NP_001314:NM_001323_1-20
MARSNLPLALGLALVAFCLL

SEQ. ID. NO.:121 HG1018388P1 NP_001314:NM_001323_1-28
MARSNLPLALGLALVAFCLLALPRDARA

SEQ. ID. NO.:122 HG1018389P1 NP_001314:NM_001323_1-21
MARSNLPLALGLALVAFCLLA

SEQ. ID. NO.:123 HG1018390P1 NP_001314:NM_001323_1-23
MARSNLPLALGLALVAFCLLALP

SEQ. ID. NO.:124 HG1018392P1 NP_001822:NM_001831_1-22
MMKTLLLFVGLLLTWESGQVLG

SEQ. ID. NO.:125 HG1018393P1 NP_001822:NM_001831_1-18
MMKTLLLFVGLLLTWESG

SEQ. ID. NO.:126 HG1018394P1 NP_001822:NM_001831_1-14
MMKTLLLFVGLLLT

SEQ. ID. NO.:127 HG1018396P1 NP_002206:NM_002215_1-24
MDGAMGPRGLLLCMYLVSLILQA

SEQ. ID. NO.:128 HG1018397P1 NP_002206:NM_002215_1-29
MDGAMGPRGLLLCMYLVSLILQAMPALG

SEQ. ID. NO.:129 HG1018398P1 NP_002206:NM_002215_1-30
MDGAMGPRGLLLCMYLVSLILQAMPALGS

SEQ. ID. NO.:130 HG1018399P1 NP_002206:NM_002215_1-23
MDGAMGPRGLLLCMYLVSLILQ

SEQ. ID. NO.:131 HG1018400P1 NP_002206:NM_002215_1-31
MDGAMGPRGLLLCMYLVSLILQAMPALGSA

SEQ. ID. NO.:132 HG1018402P1 NP_002300:NM_002309_1-22
MKVLAAGVVPLLVLHWKHGAG

SEQ. ID. NO.:133 HG1018403P1 NP_002300:NM_002309_1-23
MKVLAAGVVPLLVLHWKHGAGS

SEQ. ID. NO.:134 HG1018405P1 NP_002336:NM_002345_1-18
MSLSAFTLFLALIGGTSG

SEQ. ID. NO.:135 HG1018406P1 NP_002336:NM_002345_1-15
MSLSAFTLFLALIGG

SEQ. ID. NO.:136 HG1018407P1 NP_002336:NM_002345_1-17
MSLSAFTLFLALIGGTS

SEQ. ID. NO.:137 HG1018408P1 NP_002336:NM_002345_1-14
MSLSAFTLFLALIG

SEQ. ID. NO.:138 HG1018410P1 NP_002402:NM_002411_1-18
MKLLMVLML AALSQHCYA

SEQ. ID. NO.:139 HG1018412P1 NP_002505:NM_002514_1-30
MQSVQSTSFCLRKQCLCLTFLLHLLGQVA

SEQ. ID. NO.:140 HG1018413P1 NP_002505:NM_002514_1-32
MQSVQSTSFCLRKQCLCLTFLLHLLGQVAAT

SEQ. ID. NO.:141 HG1018414P1 NP_002505:NM_002514_1-28
MQSVQSTSFCLRKQCLCLTFLLHLLGQ

SEQ. ID. NO.:142 HG1018415P1 NP_002505:NM_002514_1-27
MQSVQSTSFCLRKQCLCLTFLLHLLG

SEQ. ID. NO.:143 HG1018416P1 NP_002505:NM_002514_1-31
MQSVQSTSFCLRKQCLCLTFLLHLLGQVAA

SEQ. ID. NO.:144 HG1018418P1 NP_002892:NM_002901_1-26
MARGGRGRRGLALGLLLALVLAAPRV

SEQ. ID. NO.:145 HG1018419P1 NP_002892:NM_002901_1-22
MARGGRGRRGLALGLLLALVL

SEQ. ID. NO.:146 HG1018420P1 NP_002892:NM_002901_1-29
MARGGRGRRGLALGLLLALVLAAPRVLRA

SEQ. ID. NO.:147 HG1018421P1 NP_002892:NM_002901_1-24
MARGGRGRRGLALGLLLALVLAP

SEQ. ID. NO.:148 HG1018422P1 NP_002892:NM_002901_1-23
MARGGRGRRGLALGLLLALVLA

SEQ. ID. NO.:149 HG1018424P1 NP_002893:NM_002902_1-25
MRLGPRTAALGLLLLCAAAAGAGKA

SEQ. ID. NO.:150 HG1018425P1 NP_002893:NM_002902_1-19
MRLGPRTAALGLLLLCAAA

SEQ. ID. NO.:151 HG1018426P1 NP_002893:NM_002902_1-22
MRLGPRTAALGLLLLCAAAAGA

SEQ. ID. NO.:152 HG1018427P1 NP_002893:NM_002902_1-18
MRLGPRTAALGLLLLCAA

SEQ. ID. NO.:153 HG1018428P1 NP_002893:NM_002902_1-20
MRLGPRTAALGLLLLCAAAA

SEQ. ID. NO.:154 HG1018429P1 NP_002893:NM_002902_1-21
MRLGPRTAALGLLLLCAAAAG

SEQ. ID. NO.:155 HG1018430P1 NP_002893:NM_002902_1-23
MRLGPRTAALGLLLLCAAAAGAG

SEQ. ID. NO.:156 HG1018432P1 NP_005133:NM_005142_1-19
MAWFALYLLSLLWATAGTS

SEQ. ID. NO.:157 HG1018433P1 NP_005133:NM_005142_1-18
MAWFALYLLSLLWATAGT

SEQ. ID. NO.:158 HG1018434P1 NP_005133:NM_005142_1-20
MAWFALYLLSLLWATAGTST

SEQ. ID. NO.:159 HG1018435P1 NP_005133:NM_005142_1-24
MAWFALYLLSLLWATAGTSTQTQS

SEQ. ID. NO.:160 HG1018436P1 NP_005133:NM_005142_1-16
MAWFALYLLSLLWATA

SEQ. ID. NO.:161 HG1018437P1 NP_005133:NM_005142_1-17
MAWFALYLLSLLWATAG

SEQ. ID. NO.:162 HG1018438P1 NP_005133:NM_005142_1-14
MAWFALYLLSLLWA

SEQ. ID. NO.:163 HG1018440P1 NP_005445:NM_005454_1-17
MHLLLFQLLVLLPLGKT

SEQ. ID. NO.:164 HG1018442P1 NP_005555:NM_005564_1-18
MPLGLLWLGLALLGALHA

SEQ. ID. NO.:165 HG1018443P1 NP_005555:NM_005564_1-20
MPLGLLWLGLALLGALHAQA

SEQ. ID. NO.:166 HG1018444P1 NP_005555:NM_005564_1-15
MPLGLLWLGLALLGA

SEQ. ID. NO.:167 HG1018446P1 NP_005690:NM_005699_1-29
MRHNWTPDLSPLWVLLLCALHVVTLVRAT

SEQ. ID. NO.:168 HG1018447P1 NP_005690:NM_005699_1-24
MRHNWTPDLSPLWVLLLCALHVVTL

SEQ. ID. NO.:169 HG1018448P1 NP_005690:NM_005699_1-28
MRHNWTPDLSPLWVLLLCALHVVTLVRA

SEQ. ID. NO.:170 HG1018450P1 NP_006560:NM_006569_1-19
ML PLTMTVLILLLLPTGQA

SEQ. ID. NO.:171 HG1018451P1 NP_006560:NM_006569_1-18
ML PLTMTVLILLLLPTGQ

SEQ. ID. NO.:172 HG1018452P1 NP_006560:NM_006569_1-21
ML PLTMTVLILLLLPTGQAAP

SEQ. ID. NO.:173 HG1018454P1 NP_006856:NM_006865_1-15
MTSILTVLICLGLSL

SEQ. ID. NO.:174 HG1018456P1 NP_036577:NM_012445_1-26
MENPSPAAALGKALCALLLATLGAAAG

SEQ. ID. NO.:175 HG1018457P1 NP_036577:NM_012445_1-25
MENPSPAAALGKALCALLLATLGAA

SEQ. ID. NO.:176 HG1018458P1 NP_036577:NM_012445_1-24
MENPSPAAALGKALCALLLATLGA

SEQ. ID. NO.:177 HG1018459P1 NP_036577:NM_012445_1-28
MENPSPAAALGKALCALLLATLGAAAGQP

SEQ. ID. NO.:178 HG1018461P1 NP_055070:NM_014255_1-20
MKGWGWLALLLGALLGTAWA

SEQ. ID. NO.:179 HG1018462P1 NP_055070:NM_014255_1-18
MKGWGWLALLLGALLGTA

SEQ. ID. NO.:180 HG1018463P1 NP_055070:NM_014255_1-16
MKGWGWLALLLGALLG

SEQ. ID. NO.:181 HG1018465P1 NP_055582:NM_014767_1-24
MRAPGCGRLVLPLLLAAAALAEG

SEQ. ID. NO.:182 HG1018466P1 NP_055582:NM_014767_1-19
MRAPGCGRLVLPLLLAAA

SEQ. ID. NO.:183 HG1018467P1 NP_055582:NM_014767_1-22
MRAPGCGRLVLPLLLAAAALA

SEQ. ID. NO.:184 HG1018468P1 NP_055582:NM_014767_1-20
MRAPGCGRLVLPLLLAAAA

SEQ. ID. NO.:185 HG1018469P1 NP_055582:NM_014767_1-26
MRAPGCGRLVLPLLLAAAALAEGDA

SEQ. ID. NO.:186 HG1018470P1 NP_055582:NM_014767_1-21
MRAPGCGRLVLPLLLAAAAL

SEQ. ID. NO.:187 HG1018472P1 NP_055697:NM_014882_1-18
MSLGQSACLFLSIARSRS

SEQ. ID. NO.:188 HG1018474P1 NP_056965:NM_015881_1-18
MQRLGATLLCLLLAAAVP

SEQ. ID. NO.:189 HG1018475P1 NP_056965:NM_015881_1-19
MQRLGATLLCLLLAAAVPT

SEQ. ID. NO.:190 HG1018476P1 NP_056965:NM_015881_1-22
MQRLGATLLCLLLAAAVPTAPA

SEQ. ID. NO.:191 HG1018477P1 NP_056965:NM_015881_1-16
MQRLGATLLCLLLAAA

SEQ. ID. NO.:192 HG1018478P1 NP_056965:NM_015881_1-21
MQRLGATLLCLLLAAAVPTAP

SEQ. ID. NO.:193 HG1018480P1 NP_057603:NM_016519_1-26
MSASKIPLFKMKDLILILCLESFA

SEQ. ID. NO.:194 HG1018481P1 NP_057603:NM_016519_1-28
MSASKIPLFKMKDLILILCLESFAVP

SEQ. ID. NO.:195 HG1018483P1 NP_149439:NM_033183_1-18
MEMFQGLLLLLLLSMGGT

SEQ. ID. NO.:196 HG1018484P1 NP_149439:NM_033183_1-20
MEMFQGLLLLLLLSMGGTWA

SEQ. ID. NO.:197 HG1018485P1 NP_149439:NM_033183_1-16
MEMFQGLLLLLLLSMG

SEQ. ID. NO.:198 HG1018487P1 NP_644808:NM_139279_1-18
MTMRSLLRTPFLCGLLWA

SEQ. ID. NO.:199 HG1018488P1 NP_644808:NM_139279_1-20
MTMRSLLRTPFLCGLLWAF C

SEQ. ID. NO.:200 HG1018489P1 NP_644808:NM_139279_1-26
MTMRSLLRTPFLCGLLWAF CAPGARA

SEQ. ID. NO.:201 HG1018490P1 NP_644808:NM_139279_1-23
MTMRSLLRTPFLCGLLWAF CAPG

SEQ. ID. NO.:202 HG1018492P1 NP_660295:NM_145252_1-13
ML LLLTLALLGGP

SEQ. ID. NO.:203 HG1018493P1 NP_660295:NM_145252_1-16
ML LLLTLALLGGPTWA

SEQ. ID. NO.:204 HG1018494P1 NP_660295:NM_145252_1-14
ML LLLTLALLGGPT

SEQ. ID. NO.:205 HG1018495P1 NP_660295:NM_145252_1-17
ML LLLTLALLGGPTWAG

SEQ. ID. NO.:206 HG1018497P1 NP_689534:NM_152321_1-25
MEAAPSRFMFLFLLTCELA AEVAA

SEQ. ID. NO.:207 HG1018498P1 NP_689534:NM_152321_1-21
MEAAPSRFMFLFLLTCELA A

SEQ. ID. NO.:208 HG1018500P1 NP_689848:NM_152635_1-18
MPPFLLLTCLFITGTSVS

SEQ. ID. NO.:209 HG1018501P1 NP_689848:NM_152635_1-16
MPPFLLLTCLFITGTS

SEQ. ID. NO.:210 HG1018502P1 NP_689848:NM_152635_1-15
MPPFLLLTCLFITGT

SEQ. ID. NO.:211 HG1018504P1 NP_689968:NM_152755_1-21
MGPVRLGILLFLFLAVHEAWA

SEQ. ID. NO.:212 HG1018506P1 NP_766630:NM_173042_1-29
MRHNWTPDLSPLWVLLLC AHVVTLLVRAT

SEQ. ID. NO.:213 HG1018507P1 NP_766630:NM_173042_1-24
MRHNWTPDLSPLWVLLLC AHVVTL

SEQ. ID. NO.:214 HG1018508P1 NP_766630:NM_173042_1-28
MRHNWTPDLSPLWVLLLC AHVVTLLVRA

SEQ. ID. NO.:215 HG1018510P1 NP_776214:NM_173842_1-23
MEICRGLRSHLITLLLFL FHSET

SEQ. ID. NO.:216 HG1018511P1 NP_776214:NM_173842_1-25
MEICRGLRSHLITLLLFL FHSETIC

SEQ. ID. NO.:217 HG1018513P1 NP_783165:NM_175575_1-32
MWAPRCRRFWSRWEQVAALLLLLLLLGVPPRS

SEQ. ID. NO.:218 HG1018514P1 NP_783165:NM_175575_1-34
MWAPRCRRFWSRWEQVAALLLLLLLLGVPPRSLA

SEQ. ID. NO.:219 HG1018515P1 NP_783165:NM_175575_1-29
MWAPRCRRFWSRWEQVAALLLLLLLLGVP

SEQ. ID. NO.:220 HG1018516P1 NP_783165:NM_175575_1-30
MWAPRCRRFWSRWEQVAALLLLLLLLGVPP

SEQ. ID. NO.:221 HG1018517P1 NP_783165:NM_175575_1-27
MWAPRCRRFWSRWEQVAALLLLLLLLG

SEQ. ID. NO.:222 HG1018857P1 27482680:27482679_1-26
MWCASPVAVVAFCAGLLVSHPVLTQG

SEQ. ID. NO.:223 HG1018858P1 27482680:27482679_1-24
MWCASPVAVVAFCAGLLVSHPVLT

nucleotide sequence chosen from:

- (a) SEQ ID NOS.:14 and 16-18;
 - (b) a polynucleotide encoding a polypeptide comprising a amino acid sequence chosen from SEQ ID NOS.:15, and 21-22;
 - (c) a complementary polynucleotide comprising a complementary nucleotide sequence that is complementary to the first nucleotide sequence of (a); and
 - (d) a biologically active fragment of any of (a) – (c); and, wherein the nucleic acid molecule is an isolated molecule.
2. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule is chosen from: a cDNA molecule, a genomic DNA molecule, a cRNA molecule, a siRNA molecule, an RNAi molecule, an mRNA molecule, an anti-sense molecule, and a ribozyme.
 3. The nucleic acid molecule of claim 1, further comprising its complement.
 4. The nucleic acid molecule of claim 1, wherein the first nucleotide sequence is SEQ ID NO.:17.
 5. The nucleic acid molecule of claim 1, wherein the first nucleotide sequence is SEQ ID NO.:18.
 6. The nucleic acid molecule of either claim 4 or 5, further comprising a second polynucleotide.
 7. The nucleic acid molecule of claim 6, wherein the second polynucleotide comprises a second nucleotide sequence encoding a secretory leader, and the secretory leader is a homologous or heterologous leader.
 8. The nucleic acid molecule of claim 7, wherein the secretory leader is a heterologous leader.
 9. The nucleic acid molecule of claim 7, wherein the secretory leader is a secretory leader chosen from SEQ ID NOS.:26-223.
 10. A polypeptide comprising a first amino acid sequence, wherein the first amino acid sequence is chosen from:
 - (a) SEQ ID NOS.:15 and 21-22;
 - (b) a sequence encoded by one of SEQ ID NOS.:14 and 16-18; and
 - (c) an active fragment of (a) or (b); wherein the polypeptide is an isolated molecule.
 11. The polypeptide of claim 10, wherein the polypeptide is present in a cell culture.

13. The polypeptide of claim 11, wherein the cell culture is chosen from a bacterial cell culture, a mammalian cell culture, an insect cell culture, and a yeast cell culture.
14. The polypeptide of claim 10, wherein the polypeptide is present in a plant or a non-human animal.
15. The polypeptide of claim 10, wherein the first amino acid sequence is the amino acid sequence of SEQ ID NO.:21.
16. The polypeptide of claim 10, wherein the first amino acid sequence is the amino acid sequence of SEQ ID NO.:22.
17. The polypeptide of claim 10, wherein the polypeptide further comprises a second amino acid sequence, and the second amino acid sequence is a secretory leader, the secretory leader is a homologous leader or a heterologous leader, and wherein the first and second amino acid sequences are operably linked.
18. The polypeptide of claim 17, wherein the secretory leader sequence is a heterologous leader sequence.
19. The polypeptide of claim 18 wherein the heterologous leader sequence is chosen from SEQ ID NOS.:26-223.
20. A polypeptide comprising at least six contiguous amino acids from SEQ ID NO.:24 or encoded by SEQ ID NO.:20.
21. A vector comprising the nucleic acid molecule of claim 1 and a promoter that regulates the expression of the nucleic acid molecule.
22. The vector of claim 21, wherein the vector is a viral vector or a plasmid.
23. The vector of claim 21, wherein the vector is a pTT vector.
24. The vector of claim 21, wherein the promoter is chosen from one that is naturally contiguous to the nucleic acid molecule and one that is not naturally contiguous to the nucleic acid molecule.
25. The vector of claim 21, wherein the promoter is chosen from an inducible promoter, a conditionally-active promoter, a constitutive promoter, and a tissue-specific promoter.
26. A recombinant host cell comprising a cell and the nucleic acid of any of claim 1, 4 or 5, the polypeptide of claim 10, 15, or 16, or the vector of claim 21.
27. The host cell of claim 26, wherein the cell is a prokaryotic cell.

cell, a non-human mammalian cell, an insect cell, a fish cell, a plant cell, and a fungal cell.

30. The host cell of claim 26, wherein the cell is a mammalian cell.

31. The host cell of claim 30, wherein the mammalian cell is a cell of a 293 cell line or a CHO cell line.

32. The host cell of claim 31, wherein the cell is a 293 cell.

33. The host cell of claim 32, wherein the 293 cell is a 293T cell or a 293E cell.

34. An animal injected with the nucleic acid molecule of claim 1 or the polypeptide of claim 10.

35. The animal of claim 34, wherein the animal is a rodent, a non-human primate, a rabbit, a dog, or a pig.

36. A nucleic acid composition comprising the nucleic acid molecule of claim 1 and a carrier.

37. A polypeptide composition comprising the polypeptide molecule of claim 10 and a carrier.

38. A vector composition comprising the vector of claim 21 and a carrier.

39. A host cell composition comprising the host cell of claim 26 and a carrier.

40. The composition of any of claims 36 – 38, wherein the carrier is a pharmaceutically acceptable carrier or excipient.

41. A host cell composition comprising a recombinant host cell comprising a cell;

a pharmaceutically acceptable carrier or excipient; and

the nucleic acid of claim 1, the polypeptide of claim 10, and/or the vector of claim 21.

42. A method of producing a recombinant host cell comprising:

(a) providing a vector that comprises the nucleic acid molecule of claim 1; and

(b) allowing a cell to come into contact with the vector to form a recombinant host cell transfected with the nucleic acid molecule.

43. A method of producing a polypeptide comprising:

(a) providing the nucleic acid of claim 1; and

(b) expressing the nucleic acid molecule in an expression system to produce the polypeptide.

45. The method of claim 44, wherein the cellular expression system is a prokaryotic or eukaryotic expression system.

46. The method of claim 43, wherein the expression system comprises a host cell transfected with the nucleic acid molecule, forming a recombinant host cell, and the method further comprises culturing the recombinant host cell to produce the polypeptide.

47. The method of claim 43, wherein the expression system is a cell-free expression system chosen from a wheat germ lysate expression system, a rabbit reticulocyte expression system, a ribosomal display, and an *E. coli* lysate expression system.

48. A polypeptide produced by the method of claim 43.

49. A polypeptide produced by the method of claim 46, wherein the host cell is chosen from a mammalian cell, an insect cell, a plant cell, a yeast cell, and a bacterial cell.

50. A method of determining the presence of an antibody specific to the polypeptide of claim 10 in a sample comprising:

- (a) providing a composition comprising the polypeptide of claim 10;
- (b) allowing the polypeptide to interact with the sample; and
- (c) determining whether interaction has occurred between the polypeptide and the antibody.

51. The antibody of claim 50, chosen from a polyclonal antibody, a monoclonal antibody, a single chain antibody, and an active fragment of any of these.

52. The antibody of claim 51, wherein the antibody is a fragment chosen from an antigen binding fragment, an Fc fragment, a cdr fragment, a V_H fragment, a V_C fragment, and a framework fragment.

53. The polypeptide of claim 10 or a polypeptide produced by the method of any of claims 43-49, wherein the polypeptide further comprises at least one fusion partner.

54. The polypeptide of claim 53, wherein the fusion partner is chosen from a polymer, a polypeptide, a succinyl group, fetuin, leucine zipper nuclear factor erythroid derivative-2 (NFE2), neuroretinal leucine zipper, mannose motif (mbp1), tetranectin, an Fc fragment, and serum albumin.

55. A method of inhibiting tumor growth comprising:

- (a) providing a composition comprising the polypeptide chosen from any one of claims 10, 15, 16, 48, and an active fragment of any of these; and

contacting tumor cells having a death domain receptor with a polypeptide chosen from any one of claims 10, 15-16, 48, and an active fragment of any of these.

57. The method of claim 56, wherein the tumor cells are human tumor cells.

58. The method of claim 57, wherein the tumor cells are solid tumor cells or leukemic tumor cells.

59. The method of claim 55, wherein tumor cells are chosen from a carcinoma, a mammary adenocarcinoma, and a non-small cell lung carcinoma.

60. The method of claim 57, wherein the tumor cells are a breast tumor, a colon tumor, a lung tumor, a prostate tumor, a bladder tumor, a stomach tumor, and skin cancer.

61. A method for treating of a mammary adenocarcinoma in a subject comprising:

(a) providing a composition containing a polypeptide chosen from any of claims 10, 15-16, 48, and an active fragment of any of these; and a pharmaceutically acceptable carrier; and

(b) administering the composition to the subject.

62. A method for treating of a non-small cell lung carcinoma in a subject comprising:

(a) providing a composition containing a polypeptide chosen from any of claims 10, 15-16, 48, and an active fragment of any of these; and a pharmaceutically acceptable carrier; and

(b) administering the composition to the subject.

63. A method for treating of a breast tumor in a subject comprising:

(a) providing a composition containing a polypeptide chosen from any of claims 10, 15-16, 48, and an active fragment of any of these; and a pharmaceutically acceptable carrier; and

(b) administering the composition to the subject.

64. A method of treating of a lung tumor in a subject comprising:

(a) providing a composition containing a polypeptide chosen from any of claims 10, 15-16, 48, and an active fragment of any of these; and a pharmaceutically acceptable carrier; and

(b) administering the composition to the subject.

65. A method of treating of a prostate tumor in a subject comprising:

acceptable carrier; and

(b) administering the composition to the subject.

66. A method of treating a colon tumor in a subject comprising:

(a) providing a composition containing a polypeptide chosen from any of claims 10, 15-16, 48, and an active fragment of any of these; and a pharmaceutically acceptable carrier; and

(b) administering the composition to the subject.

67. A method of treating a stomach tumor in a subject comprising:

(a) providing a composition containing a polypeptide chosen from any of claims 10, 15-16, 48, and an active fragment of any of these; and a pharmaceutically acceptable carrier; and

(b) administering the composition to the subject.

68. A method of treating a bladder tumor in a subject comprising:

(a) providing a composition containing a polypeptide chosen from any of claims 10, 15-16, 48, and an active fragment of any of these; and a pharmaceutically acceptable carrier; and

(b) administering the composition to the subject.

69. A method of treating of skin cancer in a subject comprising:

(a) providing a composition containing a polypeptide chosen from any of claims 10, 15-16, 48, and an active fragment of any of these, and a pharmaceutically acceptable carrier; and

(b) administering the composition to the subject.

70. A method of treating a glioblastoma in a subject comprising:

(a) providing a composition containing a polypeptide chosen from any of claims 10, 15-16, 48, and an active fragment of any of these; and a pharmaceutically acceptable carrier; and

(b) administering the composition to the subject.

71. A pharmaceutical composition comprising:

(a) a polypeptide chosen from any of claims 10, 15-16, 48, and an active fragment of any of these;

(b) an anti-cancer agent; and

chosen from a chemotherapeutic agent, a radiotherapeutic agent, an anti-angiogenic agent, and an apoptosis-inducing agent.

73. The pharmaceutical composition of claim 72, wherein the chemotherapeutic agent is chosen from a steroid, a cytokine, a cytosine arabinoside, fluorouracil, methotrexate, aminopterin, an anthracycline, mitomycin C, a vinca alkaloid, an antibiotic, demecolcine, etoposide, mithramycin, chlorambucil, and melphalan.

74. A method of treating a tumor in a subject comprising:

(a) providing a first composition comprising fragments of mature APO2L polypeptide;

(b) providing a second composition comprising an anti-cancer agent different from the polypeptide of 10; and

(c) administering the first and second compositions to the subject.

75. The method of claim 74, wherein the second composition comprises a monoclonal antibody composition or a chemotherapeutic agent or another polypeptide.

76. The method of claim 74, wherein the second composition reduces expression of Akt or survivin.

77. The method of claim 76, wherein the Akt inhibitor is SH-6.

78. The method of 76, wherein the tumor is a glioma or glioblastoma.

79. The method of claim 74, wherein the tumor is a multidrug resistant tumor.

80. The method of claim 79, wherein the multidrug resistant tumor is an osteosarcoma.

81. The method of claim 74, wherein the second composition comprises another polypeptide.

82. The method of claim 81, wherein the other polypeptide is an interferon.

83. The method of claim 82, wherein the interferon is interferon gamma.

84. The method of claim 83, wherein the tumor is Ewing's sarcoma.

85. The method of claim 74, wherein the second composition comprises a chemotherapeutic agent.

86. The method of claim 85, wherein the chemotherapeutic agent is doxorubicin, epirubicin, pirarubicin, or cisplatin.

87. The method of claim 86, wherein the tumor is prostate cancer.

89. The method of claim 88, wherein the inhibitor of NF- κ B is N-acetyl-L-leuciny-L-leuciny-Lnorleucinal (LLnL).

90. The method of claim 74, wherein the fragments comprises amino acid residues 40 – 45 and 92 – 281, 92 – 281, or 114 – 281 of the full length wild type APO2L polypeptide.